

<110> Presnell, Scott R.
Kindsvogel, Wayne

<130> 99-106

<151> 1999-12-23

<151> 2000-12-01

<170> FastSEQ for Windows Version 3.0

<213> Homo sapiens

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 Leu Met Gly Thr Leu Ala Thr Ser Cys Leu Leu Leu Leu Ala Leu Leu
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gta cag gga gga gca gct gcg ccc atc agc tcc cac tgc agg ctt gac 149
Val Gln Gly Gly Ala Ala Ala Pro Ile Ser Ser His Cys Arg Leu Asp
30 35 40

aag tcc aac ttc cag cag ccc tat atc acc aac cgc acc ttc atg ctg 197
Lys Ser Asn Phe Gln Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu
45 50 55

gct aag gag gct agc ttg gct gat aac aac aca gac gtt cgt ctc att 245
Ala Lys Glu Ala Ser Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile
60 65 70 75

ggg gag aaa ctg ttc cac gga gtc agt atg agt gag cgc tgc tat ctg 293
Gly Glu Lys Leu Phe His Gly Val Ser Met Ser Glu Arg Cys Tyr Leu
80 85 90

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Met Lys Gln Val Leu Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln
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tct gat agg ttc cag cct tat atg cag gag gtg gtg ccc ttc ctg gcc 389
Ser Asp Arg Phe Gln Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala
110 115 120

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Arg Leu Ser Asn Arg Leu Ser Thr Cys His Ile Glu Gly Asp Asp Leu
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cat atc cag agg aat gtg caa aag ctg aag gac aca gtg aaa aag ctt 485
His Ile Gln Arg Asn Val Gln Lys Leu Lys Asp Thr Val Lys Lys Leu
140 145 150 155

gga gag agt gga gag atc aaa gca att gga gaa ctg gat ttg ctg ttt 533
Gly Glu Ser Gly Glu Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe
160 165 170

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Met Ser Leu Arg Asn Ala Cys Ile
175

taaccccctt tccctgctag aaataacaat tagatgcccc aaagcgattt tttttaacca 647
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35 40 45
Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser
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His Gly Val Ser Met Ser Glu Arg Cys Tyr Leu Met Lys Gln Val Leu
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Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln Ser Asp Arg Phe Gln
100 105 110
Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala Arg Leu Ser Asn Arg
115 120 125
Leu Ser Thr Cys His Ile Glu Gly Asp Asp Leu His Ile Gln Arg Asn
130 135 140
Val Gln Lys Leu Lys Asp Thr Val Lys Lys Leu Gly Glu Ser Gly Glu
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Ala Cys Ile

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 35 40 45
 Lys Glu Ala Ser Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly
 50 55 60
 Glu Lys Leu Phe His Gly Val Ser Met Ser Glu Arg Cys Tyr Leu Met
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 Lys Gln Val Leu Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln Ser
 85 90 95
 Asp Arg Phe Gln Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala Arg
 100 105 110
 Leu Ser Asn Arg Leu Ser Thr Cys His Ile Glu Gly Asp Asp Leu His
 115 120 125
 Ile Gln Arg Asn Val Gln Lys Leu Lys Asp Thr Val Lys Lys Leu Gly
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 acnaaymgna cnttyatgyt ngcnaargar gcwnsnytng cngayaayaa yacngaygt 180
 mgnytnathg gngaraaryt nttycayggg gtnwsnatgw sngarmgntg ytayytnatg 240
 aarcargtny tnaayttyac nytngargar gtnytnttyc cncarwsnga ymgnttycar 300
 ccntayatgc argargtngt nccnttyytn gcnmgnytnw snaaymgnyt nwsnacntgy 360
 cayathgarg gngaygayyt ncayathcar mgnaaygtnc araarytnaa rgayacngtn 420
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Leu Thr Val Gly Ser Leu Ala Ala His Ala Pro Glu Asp Pro Ser Asp
10 15 20

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Leu Leu Gln His Val Lys Phe Gln Ser Ser Asn Phe Glu Asn Ile Leu
25 30 35

acg tgg gac agc ggg cca gag ggc acc cca gac acg gtc tac agc atc 198
Thr Trp Asp Ser Gly Pro Glu Gly Thr Pro Asp Thr Val Tyr Ser Ile
40 45 50 55

gag tat aag acg tac gga gag agg gac tgg gtg gca aag aag ggc tgt 246

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Gln	Arg	Ile	Thr	Arg	Lys	Ser	Cys	Asn	Leu	Thr	Val	Glu	Thr	Gly	Asn	
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Leu	Thr	Glu	Leu	Tyr	Tyr	Ala	Arg	Val	Thr	Ala	Val	Ser	Ala	Gly	Gly	
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Arg	Ser	Ala	Thr	Lys	Met	Thr	Asp	Arg	Phe	Ser	Ser	Leu	Gln	His	Thr	
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acc	ctc	aag	cca	cct	gat	gtg	acc	tgt	atc	tcc	aaa	gtg	aga	tcg	att	438
Thr	Leu	Lys	Pro	Pro	Asp	Val	Thr	Cys	Ile	Ser	Lys	Val	Arg	Ser	Ile	
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Gln	Met	Ile	Val	His	Pro	Thr	Pro	Thr	Pro	Ile	Arg	Ala	Gly	Asp	Gly	
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cac	cgg	cta	acc	ctg	gaa	gac	atc	ttc	cat	gac	ctg	ttc	tac	cac	tta	534
His	Arg	Leu	Thr	Leu	Glu	Asp	Ile	Phe	His	Asp	Leu	Phe	Tyr	His	Leu	
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Glu	Leu	Gln	Val	Asn	Arg	Thr	Tyr	Gln	Met	His	Leu	Gly	Gly	Lys	Gln	
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acc	atc	atg	att	tgc	gtt	ccc	acc	tgg	gcc	aag	gag	agt	gcc	ccc	tac	678
Thr	Ile	Met	Ile	Cys	Val	Pro	Thr	Trp	Ala	Lys	Glu	Ser	Ala	Pro	Tyr	
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Met	Cys	Arg	Val	Lys	Thr	Leu	Pro	Asp	Arg	Thr	Trp	Thr	Tyr	Ser	Phe	
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Gly Gln Pro Asp Ile Ser Ile Leu Gln Pro Ser Asn Val Pro Pro Pro	
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Gln Ile Leu Ser Pro Leu Ser Tyr Ala Pro Asn Ala Ala Pro Glu Val	
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Gly Pro Pro Ser Tyr Ala Pro Gln Val Thr Pro Glu Ala Gln Phe Pro	
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Phe Tyr Ala Pro Gln Ala Ile Ser Lys Val Gln Pro Ser Ser Tyr Ala	
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His Leu Arg Pro Lys Gly Gln Leu Gln Lys Glu Pro Pro Ala Gly Ser	
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Asp Leu Glu Gln Pro Thr Glu Leu Asp Ser Leu Phe Arg Gly Leu Ala	
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Leu Thr Val Gln Trp Glu Ser
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Trp Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn
65           70           75           80
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 485 490 495
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 Leu Gln Pro Pro Ser Gly Pro Cys Ser Pro Ser Asp Gln Gly Pro Ser
 515 520 525
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cacacaggcg cgcctcaa at gcaggcattt ctcagag

37

<210> 22

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<223> Oligonucleotide primer ZC14666

<400> 22

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18

<210> 23

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<400> 23

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22

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<223> Oligonucleotide primer ZC25963

<400> 24

agtcaacgca tgagtctctg aag

23

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<223> Oligonucleotide primer ZC28354

<400> 25

accaacaaag agccattgac ttg

23

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<223> Oligonucleotide primer ZC21195

<400> 26

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23

<210> 27

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23

<210> 28

<211> 25

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<223> Oligonucleotide primer ZC14063

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caccagacat aatagctgac agact

25

<210> 29

<211> 21

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<223> Oligonucleotide primer ZC17574

<400> 29

ggtrttgctc agcatgcaca c

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<212> DNA

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<223> Oligonucleotide primer ZC17600

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<210> 32

<211> 2149

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(693)

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 Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu
 1 5 10 15

48

act ggt gta gca gga act cag tca acg cat gag tct ctg aag cct cag
 Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln
 20 25 30

96

agg gta caa ttt cag tcc cga aat ttt cac aac att ttg caa tgg cag
 Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln
 35 40 45

144

cct ggg agg gca ctt act ggc aac agc agt gtc tat ttt gtg cag tac

192

Pro	Gly	Arg	Ala	Leu	Thr	Gly	Asn	Ser	Ser	Val	Tyr	Phe	Val	Gln	Tyr		
50						55					60						
aaa	ata	tat	gga	cag	aga	caa	tgg	aaa	aat	aaa	gaa	gac	tgt	tgg	ggt	240	
Lys	Ile	Tyr	Gly	Gln	Arg	Gln	Trp	Lys	Asn	Lys	Glu	Asp	Cys	Trp	Gly		
65					70					75					80		
act	caa	gaa	ctc	tct	tgt	gac	ctt	acc	agt	gaa	acc	tca	gac	ata	cag	288	
Thr	Gln	Glu	Leu	Ser	Cys	Asp	Leu	Thr	Ser	Glu	Thr	Ser	Asp	Ile	Gln		
				85				90						95			
gaa	cct	tat	tac	ggg	agg	gtg	agg	gcg	gcc	tcg	gct	ggg	agc	tac	tca	336	
Glu	Pro	Tyr	Tyr	Gly	Arg	Val	Arg	Ala	Ala	Ser	Ala	Gly	Ser	Tyr	Ser		
			100					105					110				
gaa	tgg	agc	atg	acg	ccg	cgg	ttc	act	ccc	tgg	tgg	gaa	aca	aaa	ata	384	
Glu	Trp	Ser	Met	Thr	Pro	Arg	Phe	Thr	Pro	Trp	Trp	Glu	Thr	Lys	Ile		
		115					120					125					
gat	cct	cca	gtc	atg	aat	ata	acc	caa	gtc	aat	ggc	tct	ttg	ttg	gta	432	
Asp	Pro	Pro	Val	Met	Asn	Ile	Thr	Gln	Val	Asn	Gly	Ser	Leu	Leu	Val		
	130					135					140						
att	ctc	cat	gct	cca	aat	tta	cca	tat	aga	tac	caa	aag	gaa	aaa	aat	480	
Ile	Leu	His	Ala	Pro	Asn	Leu	Pro	Tyr	Arg	Tyr	Gln	Lys	Glu	Lys	Asn		
145					150					155					160		
gta	tct	ata	gaa	gat	tac	tat	gaa	cta	cta	tac	cga	gtt	ttt	ata	att	528	
Val	Ser	Ile	Glu	Asp	Tyr	Tyr	Glu	Leu	Leu	Tyr	Arg	Val	Phe	Ile	Ile		
				165				170						175			
aac	aat	tca	cta	gaa	aag	gag	caa	aag	gtt	tat	gaa	ggg	gct	cac	aga	576	
Asn	Asn	Ser	Leu	Glu	Lys	Glu	Gln	Lys	Val	Tyr	Glu	Gly	Ala	His	Arg		
			180					185					190				
gcg	gtt	gaa	att	gaa	gct	cta	aca	cca	cac	tcc	agc	tac	tgt	gta	gtg	624	
Ala	Val	Glu	Ile	Glu	Ala	Leu	Thr	Pro	His	Ser	Ser	Tyr	Cys	Val	Val		
		195				200						205					
gct	gaa	ata	tat	cag	ccc	atg	tta	gac	aga	aga	agt	cag	aga	agt	gaa	672	
Ala	Glu	Ile	Tyr	Gln	Pro	Met	Leu	Asp	Arg	Arg	Ser	Gln	Arg	Ser	Glu		
	210					215					220						

gag aga tgt gtg gaa att cca tgacttggtg aatttggtcat tcagcaatgt 723
 Glu Arg Cys Val Glu Ile Pro
 225 230

ggaaattcta aagctccctg agaacaggat gactcgtgtt tgaaggatct tattttaaatt 783
 tgtttttgta ttttcttaaa gcaatattca ctgttacacc ttggggactt ctttgtttat 843
 ccattctttt atcctttata tttcatttta aactataatt gaacgacatt cccccgaaa 903
 aattgaaatg taaagatgag gcagagaata aagtgttcta tgaaattcag aactttattt 963
 ctgaatgtaa catccctaatt aacaaccttc attcttctaa tacagcaaaa taaaaattta 1023
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 caacagaaag ctgccttctt cacttgaggc taagtcttca tatatgttta aggttgtctt 1863
 tctagtgagg agatacatat cagagaacat ttgtacaatt ccccatgaaa attgctccaa 1923
 agttgataac aatatagtcg gtgcttctag ttatatgcaa gtactcagtg ataaatggat 1983
 taaaaaatat tcagaaatgt attggggggt ggaggagaat aagaggcaga gcaagagcta 2043
 gagaattggt ttccttgctt ccctgtatgc tcagaaaaca ttgatttgag catagacgca 2103
 gagactgaaa aaaaaaaaaat gctcgagcgg ccgccatatc cttggt 2149

<210> 33

<211> 231

<212> PRT

<213> Homo sapiens

<400> 33

Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu
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 Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln
 20 25 30
 Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln
 35 40 45
 Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr
 50 55 60

Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly
 65 70 75 80
 Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln
 85 90 95
 Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser
 100 105 110
 Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile
 115 120 125
 Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val
 130 135 140
 Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn
 145 150 155 160
 Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile
 165 170 175
 Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg
 180 185 190
 Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val
 195 200 205
 Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu
 210 215 220
 Glu Arg Cys Val Glu Ile Pro
 225 230

<210> 34

<211> 29

<212> PRT

<213> Artificial Sequence

<220>

<223> Human ZCYT018 peptide 1 (huZCYT018-1)

<400> 34

Lys Glu Ala Ser Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly
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 Glu Lys Leu Phe His Gly Val Ser Met Ser Glu Arg Cys
 20 25

<210> 35

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> Human ZCYT018 peptide 2 (huZCYT018-2)

<400> 35

Glu	Glu	Val	Leu	Phe	Pro	Gln	Ser	Asp	Arg	Phe	Gln	Pro	Tyr	Met	Gln
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Glu	Val	Val	Pro	Cys											
			20												

<210> 36

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Human ZCYT018 peptide 3 (huZCYT018-3)

<400> 36

Cys	Asn	Val	Gln	Lys	Leu	Lys	Asp	Thr	Val	Lys	Lys	Leu	Gly	Glu	Ser
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Gly	Glu	Ile	Lys	Ala	Ile	Gly	Glu								
			20												

<210> 37

<211> 778

<212> DNA

<213> mus musculus

<220>

<221> CDS

<222> (47)...(583)

<400> 37

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						Met	Ala	Val								
						1										
ctg	cag	aaa	tct	atg	agt	ttt	tcc	ctt	atg	ggg	act	ttg	gcc	gcc	agc	103
Leu	Gln	Lys	Ser	Met	Ser	Phe	Ser	Leu	Met	Gly	Thr	Leu	Ala	Ala	Ser	
		5					10					15				
tgc	ctg	ctt	ctc	att	gcc	ctg	tgg	gcc	cag	gag	gca	aat	gcg	ctg	ccc	151
Cys	Leu	Leu	Leu	Ile	Ala	Leu	Trp	Ala	Gln	Glu	Ala	Asn	Ala	Leu	Pro	
		20				25				30					35	

gtc aac acc cgg tgc aag ctt gag gtg tcc aac ttc cag cag ccg tac 199
 Val Asn Thr Arg Cys Lys Leu Glu Val Ser Asn Phe Gln Gln Pro Tyr
 40 45 50

atc gtc aac cgc acc ttt atg ctg gcc aag gag gcc agc ctt gca gat 247
 Ile Val Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser Leu Ala Asp
 55 60 65

aac aac aca gat gtc cgg ctc atc ggg gag aaa ctg ttc cga gga gtc 295
 Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe Arg Gly Val
 70 75 80

aat gct aag gat cag tgc tac ctg atg aag cag gtg ctc aac ttc acc 343
 Asn Ala Lys Asp Gln Cys Tyr Leu Met Lys Gln Val Leu Asn Phe Thr
 85 90 95

ctg gaa gac gtt ctg ctc ccc cag tca gac agg ttc cag ccc tac atg 391
 Leu Glu Asp Val Leu Leu Pro Gln Ser Asp Arg Phe Gln Pro Tyr Met
 100 105 110 115

cag gag gtg gtg cct ttc ctg acc aaa ctc agc aat cag ctc agc tcc 439
 Gln Glu Val Val Pro Phe Leu Thr Lys Leu Ser Asn Gln Leu Ser Ser
 120 125 130

tgt cac atc agc ggt gac gac cag aac atc cag aag aat gtc aga agg 487
 Cys His Ile Ser Gly Asp Asp Gln Asn Ile Gln Lys Asn Val Arg Arg
 135 140 145

ctg aag gag aca gtg aaa aag ctt gga gag agt gga gag atc aag gcg 535
 Leu Lys Glu Thr Val Lys Lys Leu Gly Glu Ser Gly Glu Ile Lys Ala
 150 155 160

att ggg gaa ctg gac ctg ctg ttt atg tct ctg aga aat gct tgc gtc 583
 Ile Gly Glu Leu Asp Leu Leu Phe Met Ser Leu Arg Asn Ala Cys Val
 165 170 175

tgagcgagaa gaagctagaa aacgaagaac tgctccttcc tgccttctaa aaagaacaat 643
 aagatccctg aatggacttt ttactaaag gaaagtgaga agctaacgtc catcatcatt 703
 agaagatttc acatgaaacc tggctcagtt gaaaaagaaa atagtgtcaa gttgtccatg 763
 agaccagagg tagac 778

<211> 179
 <212> PRT
 <213> mus musculus

<400> 38

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Ala	Ala	Ser	Cys	Leu	Leu	Leu	Ile	Ala	Leu	Trp	Ala	Gln	Glu	Ala	Asn
			20					25					30		
Ala	Leu	Pro	Val	Asn	Thr	Arg	Cys	Lys	Leu	Glu	Val	Ser	Asn	Phe	Gln
		35					40					45			
Gln	Pro	Tyr	Ile	Val	Asn	Arg	Thr	Phe	Met	Leu	Ala	Lys	Glu	Ala	Ser
	50					55					60				
Leu	Ala	Asp	Asn	Asn	Thr	Asp	Val	Arg	Leu	Ile	Gly	Glu	Lys	Leu	Phe
65					70				75						80
Arg	Gly	Val	Asn	Ala	Lys	Asp	Gln	Cys	Tyr	Leu	Met	Lys	Gln	Val	Leu
				85				90						95	
Asn	Phe	Thr	Leu	Glu	Asp	Val	Leu	Leu	Pro	Gln	Ser	Asp	Arg	Phe	Gln
			100					105					110		
Pro	Tyr	Met	Gln	Glu	Val	Val	Pro	Phe	Leu	Thr	Lys	Leu	Ser	Asn	Gln
		115					120					125			
Leu	Ser	Ser	Cys	His	Ile	Ser	Gly	Asp	Asp	Gln	Asn	Ile	Gln	Lys	Asn
	130					135					140				
Val	Arg	Arg	Leu	Lys	Glu	Thr	Val	Lys	Lys	Leu	Gly	Glu	Ser	Gly	Glu
145					150					155					160
Ile	Lys	Ala	Ile	Gly	Glu	Leu	Asp	Leu	Leu	Phe	Met	Ser	Leu	Arg	Asn
				165				170						175	
Ala	Cys	Val													

<210> 39
 <211> 32
 <212> DNA
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<220>
 <223> Oligonucleotide primer ZC37125

<400> 39

ctatttggcc ggccaccatg gctgtcctgc ag

<210> 40
 <211> 32
 <212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC37126

<400> 40

cgtagggcg cgcctcagac gcaagcattt ct

32

<210> 41

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC28348

<400> 41

cgggatcccg atggccgccc tgcag

25

<210> 42

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC28345

<400> 42

gctctagacc aatgcaggca tttctcag

28

<210> 43

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC447

<400> 43

taacaatttc acacagg

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<210> 44

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC976

<400> 44

cgttgtaaaa cgacggcc